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                    RAW SEQUENCE LISTING          DATE: 06/05/2000
                    PATENT APPLICATION:  US/09/142,108A     TIME: 11:41:24

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                    Output Set: N:\CRF3\06022000\I142108A.raw
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    4 <110> APPLICANT: International Flower Developments Pty Ltd
    6 <120> TITLE OF INVENTION: Genetic sequences encoding flavonoid pathway enzymes
    7        and uses therefor
    9 <130> FILE REFERENCE: 2088133
   11 <140> CURRENT APPLICATION NUMBER: 09/142108A
C--> 12 <141> CURRENT FILING DATE: 1999-03-29
   14 <150> PRIOR APPLICATION NUMBER: PN8386
   15 <151> PRIOR FILING DATE: 1996-03-01
   17 <160> NUMBER OF SEQ ID NOS: 41
   19 <170> SOFTWARE: PatentIn Ver. 2.1
   21 <210> SEQ ID NO: 1
   22 <211> LENGTH: 1789
   23 <212> TYPE: DNA
   24 <213> ORGANISM: Petunia x hybrida
   26 <220> FEATURE:
   27 <221> NAME/KEY: CDS
   28 <222> LOCATION: (50)..(1588)
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   32                                                        Met Glu Ile
   33                                                          1
   35 tta agc cta att ctg tac acc gtc att ttc tca ttt ctt cta caa ttc 106
   36 Leu Ser Leu Ile Leu Tyr Thr Val Ile Phe Ser Phe Leu Leu Gln Phe
   37       5                    10                  15
   39 att ctt aga tca ttt ttc cgt aaa cgt tac cct tta cca tta cca cca 154
   40 Ile Leu Arg Ser Phe Phe Arg Lys Arg Tyr Pro Leu Pro Leu Pro Pro
   41  20                  25                  30                  35
   43 ggt cca aaa cca tgg cca att ata gga aac cta gtc cat ctt gga ccc 202
   44 Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His Leu Gly Pro
   45                  40                  45                  50
   47 aaa cca cat caa tca act gca gcc atg gct caa act tat gga cca ctc 250
   48 Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr Gly Pro Leu
   49              55                  60                  65
   51 atg tat ctt aag atg ggg ttc gta gac gtg gtg gtt gca gcc tcg gca 298
   52 Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala Ala Ser Ala
   53          70                  75                  80
   55 tcg gtt gca gct cag ttc ttg aaa act cat gat gct aat ttc tcg agc 346
   56 Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn Phe Ser Ser
   57      85                  90                  95
   59 cgt cca cca aat tct ggt gca gaa cat atg gct tat aat tat cag gat 394
   60 Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn Tyr Gln Asp
   61 100                 105                 110                 115
   63 ctt gtt ttt gca cct tat gga cct aga tgg cgt atg ctt agg aaa att 442
   64 Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu Arg Lys Ile
   65                 120                 125                 130
   67 tgc tca gtt cac ctt ttc tct acc aag gct tta gat gac ttc cgc cat 490
   68 Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp Phe Arg His
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RAW SEQUENCE LISTING
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69                135                140                145
71 gtc cgc cag gat gaa gtg aaa aca ctg acg cgc gca cta gca agt gca    538
72 Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu Ala Ser Ala
73          150                155                160
75 ggc caa aag cca gtc aaa tta ggt cag tta ttg aac gtg tgc acg acg    586
76 Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val Cys Thr Thr
77          165                170                175
79 aac gca ctc gcg cga gta atg cta ggt aag cga gta ttt gcc gac gga    634
80 Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe Ala Asp Gly
81 180                185                190                195
83 agt ggc gat gtt gat cca caa gcg gcg gag ttc aag tca atg gtg gtg    682
84 Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser Met Val Val
85          200                205                210
87 gaa atg atg gta gtc gcc ggt gtt ttt aac att ggt gat ttt att ccg    730
88 Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp Phe Ile Pro
89          215                220                225
91 caa ctt aat tgg tta gat att caa ggt gta gcc gct aaa atg aag aag    778
92 Gln Leu Asn Trp Leu Asp Ile Gln Gly Val Ala Ala Lys Met Lys Lys
93          230                235                240
95 ctc cac gcg cgt ttc gac gcg ttc ttg act gat ata ctt gaa gag cat    826
96 Leu His Ala Arg Phe Asp Ala Phe Leu Thr Asp Ile Leu Glu Glu His
97          245                250                255
99 aag ggt aaa att ttt gga gaa atg aaa gat ttg ttg agt act ttg atc    874
100 Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser Thr Leu Ile
101 260                265                270                275
103 tct ctt aaa aat gat gat gcg gat aat gat gga ggg aaa ctc act gat    922
104 Ser Leu Lys Asn Asp Asp Ala Asp Asn Asp Gly Gly Lys Leu Thr Asp
105          280                285                290
107 aca gaa att aaa gca tta ctt ttg aac ttg ttt gta gct gga aca gac    970
108 Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Val Ala Gly Thr Asp
109          295                300                305
111 aca tct tct agt aca gtt gaa tgg gcc att gct gag ctt att cgt aat   1018
112 Thr Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg Asn
113          310                315                320
115 cca aaa ata cta gcc caa gcc cag caa gag atc gac aaa gtc gtt gga   1066
116 Pro Lys Ile Leu Ala Gln Ala Gln Gln Glu Ile Asp Lys Val Val Gly
117          325                330                335
119 agg gac cgg cta gtt ggc gaa ttg gac cta gcc caa ttg aca tac ttg   1114
120 Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu Thr Tyr Leu
121 340                345                350                355
123 gaa gct ata gtc aag gaa acc ttt cgg ctt cat cca tca acc cct ctt   1162
124 Glu Ala Ile Val Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu
125          360                365                370
127 tca ctt cct aga att gca tct gag agt tgt gag atc aat ggc tat ttc   1210
128 Ser Leu Pro Arg Ile Ala Ser Glu Ser Cys Glu Ile Asn Gly Tyr Phe
129          375                380                385
131 att cca aaa ggc tca acg ctt ctc ctt aat gtt tgg gcc att gct cgt   1258
132 Ile Pro Lys Gly Ser Thr Leu Leu Leu Asn Val Trp Ala Ile Ala Arg
133          390                395                400
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135 gat cca aat gca tgg gct gat cca ttg gag ttt agg cct gaa agg ttt 1306
136 Asp Pro Asn Ala Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe
137     405                 410                 415
139 ttg cca gga ggt gag aag ccc aaa gtt gat gtc cgt ggg aat gac ttt 1354
140 Leu Pro Gly Gly Glu Lys Pro Lys Val Asp Val Arg Gly Asn Asp Phe
141 420                 425                 430                 435
143 gaa gtc ata cca ttt gga gct gga cgt agg att tgt gct gga atg aat 1402
144 Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Asn
145                 440                 445                 450
147 ttg ggt ata cgt atg gtc cag ttg atg att gca act tta ata cat gca 1450
148 Leu Gly Ile Arg Met Val Gln Leu Met Ile Ala Thr Leu Ile His Ala
149                 455                 460                 465
151 ttt aac tgg gat ttg gtc agt gga caa ttg ccg gag atg ttg aat atg 1498
152 Phe Asn Trp Asp Leu Val Ser Gly Gln Leu Pro Glu Met Leu Asn Met
153             470                 475                 480
155 gaa gaa gca tat ggg ctg acc tta caa cgg gct gat cca ttg gtt gtg 1546
156 Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro Leu Val Val
157     485                 490                 495
159 cac cca agg cct cgc tta gaa gcc caa gcg tac att ggg tga         1588
160 His Pro Arg Pro Arg Leu Glu Ala Gln Ala Tyr Ile Gly
161 500                 505                 510
163 gcagcaacag cccatggaga taacatgagt gttaaatgta tgagtctcca tatcttgttt 1648
165 agtttgttta tgctttggat ttagtagttt ttatattgat agatcaatgt ttgcattgtc 1708
167 agtaagaata tccgttgctt gtttcattaa ctccaggtgg acaataaaag aagtaatttg 1768
169 tatgaaaaaa aaaaaaaaa a                                           1789
172 <210> SEQ ID NO: 2
173 <211> LENGTH: 512
174 <212> TYPE: PRT
175 <213> ORGANISM: Petunia x hybrida
177 <400> SEQUENCE: 2
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180 Leu Gln Phe Ile Leu Arg Ser Phe Phe Arg Lys Arg Tyr Pro Leu Pro
181             20                 25                 30
182 Leu Pro Pro Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His
183             35                 40                 45
184 Leu Gly Pro Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr
185     50                 55                 60
186 Gly Pro Leu Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala
187  65                 70                 75                 80
188 Ala Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn
189             85                 90                 95
190 Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn
191             100                105                110
192 Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu
193     115                120                125
194 Arg Lys Ile Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp
195     130                135                140
196 Phe Arg His Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu
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197 145                 150                 155                 160
198 Ala Ser Ala Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val
199                 165                 170                 175
200 Cys Thr Thr Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe
201                 180                 185                 190
202 Ala Asp Gly Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser
203                 195                 200                 205
204 Met Val Val Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp
205         210                 215                 220
206 Phe Ile Pro Gln Leu Asn Trp Leu Asp Ile Gln Gly Val Ala Ala Lys
207 225                 230                 235                 240
208 Met Lys Lys Leu His Ala Arg Phe Asp Ala Phe Leu Thr Asp Ile Leu
209                 245                 250                 255
210 Glu Glu His Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser
211                 260                 265                 270
212 Thr Leu Ile Ser Leu Lys Asn Asp Asp Ala Asp Asn Asp Gly Gly Lys
213                 275                 280                 285
214 Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Val Ala
215         290                 295                 300
216 Gly Thr Asp Thr Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu
217 305                 310                 315                 320
218 Ile Arg Asn Pro Lys Ile Leu Ala Gln Ala Gln Gln Glu Ile Asp Lys
219                 325                 330                 335
220 Val Val Gly Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu
221                 340                 345                 350
222 Thr Tyr Leu Glu Ala Ile Val Lys Glu Thr Phe Arg Leu His Pro Ser
223                 355                 360                 365
224 Thr Pro Leu Ser Leu Pro Arg Ile Ala Ser Glu Ser Cys Glu Ile Asn
225         370                 375                 380
226 Gly Tyr Phe Ile Pro Lys Gly Ser Thr Leu Leu Leu Asn Val Trp Ala
227 385                 390                 395                 400
228 Ile Ala Arg Asp Pro Asn Ala Trp Ala Asp Pro Leu Glu Phe Arg Pro
229                 405                 410                 415
230 Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Lys Val Asp Val Arg Gly
231                 420                 425                 430
232 Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala
233         435                 440                 445
234 Gly Met Asn Leu Gly Ile Arg Met Val Gln Leu Met Ile Ala Thr Leu
235         450                 455                 460
236 Ile His Ala Phe Asn Trp Asp Leu Val Ser Gly Gln Leu Pro Glu Met
237 465                 470                 475                 480
238 Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro
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245 <210> SEQ ID NO: 3
246 <211> LENGTH: 1745
247 <212> TYPE: DNA
248 <213> ORGANISM: Dianthus caryophyllus
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                VERIFICATION SUMMARY              DATE: 06/05/2000
                PATENT APPLICATION:  US/09/142,108A     TIME: 11:41:26

                Input Set : A:\PTO.txt
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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:955 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:959 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:963 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:967 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:971 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:975 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:979 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:983 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:987 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:991 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:995 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:999 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1003 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1007 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1011 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1015 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1019 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1023 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1027 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1031 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1035 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1039 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1043 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1047 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1051 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1054 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 9, CDS LOCATION:3421..3907
L:1055 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:2833 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
L:2838 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
L:2843 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
L:2848 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
L:2853 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:2878 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:2883 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:2888 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:2893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:2905 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:2910 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:2915 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:2920 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
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L:2931 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:2936 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:2941 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:2946 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:2957 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36
L:2957 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36
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VERIFICATION SUMMARY                    DATE: 06/05/2000
PATENT APPLICATION:   US/09/142,108A     TIME: 11:41:26

Input Set : A:\PTO.txt
Output Set: N:\CRF3\06022000\I142108A.raw
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L:2957 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
L:2969 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:2974 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:2979 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:2984 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:2989 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:2994 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:2999 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:3004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
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L:3078 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:3083 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
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US 0914210813P1

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Indexing Officer: PTANG - PHUONG-THAO TANG
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1	CTRS	5

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